Amendments to the Claims

1. (original): A method of modifying an antibiotic-producing strain of *Streptomyces coelicolor* or *Streptomyces lividans* to increase antibiotic production in said strain, the method comprising functionally deleting in said strain the *scbA* gene.
2. (original): A method of producing an antibiotic, the method comprising providing a modified *Streptomyces* strain of claim 1, and culturing said strain under conditions suitable for production of antibiotic.
3. (previously presented): The method of claim 2, further comprising the step of purifying the antibiotic from the culture medium.
4. (original): The method of claim 3, further comprising the step of formulating the antibiotic as a pharmaceutical.
5. (original): A method of modifying an antibiotic-producing strain of a *Streptomyces coelicolor* to alter the timing of antibiotic production in said strain, the method comprising functionally deleting in said strain the *scbR* gene.
6. (original): A method of producing an antibiotic, the method comprising providing a modified *Streptomyces* strain of claim 5, and culturing said strain under conditions suitable for production of antibiotic.
7. (previously presented): The method of claim 6, further comprising the step of purifying the antibiotic from the culture medium.
8. (original): The method of claim 7, further comprising the step of formulating the antibiotic as a pharmaceutical.

9. (original): A modified strain of *Streptomyces coelicolor* or *Streptomyces lividans*, the modified strain having a functional deletion of the *scbA* gene, whereby production of at least one antibiotic in said modified strain is increased compared to a wild-type strain of *Streptomyces coelicolor* or *Streptomyces lividans*, respectively.

10. (original): A modified strain of *Streptomyces coelicolor*, the modified strain having a functional deletion of the *scbR* gene, whereby the timing of production of at least one antibiotic in said modified strain is altered compared to a wild-type strain of *Streptomyces coelicolor*.

11. (original): The method of claim 1, wherein the strain is *S. coelicolor* A3(2) or *S. lividans* 66.

12. (original): The method of claim 5, wherein the strain is *S. coelicolor* A3(2).

13. (original): The strain of claim 9, which is a modified strain of *S. coelicolor* A3(2) or *S. lividans* 66.

14. (original): The strain of claim 10, which is a modified strain of *S. coelicolor* A3(2).

15. (original): A method for identifying *Streptomyces* species in which antibiotic production is increased by functionally deleting the *scbA* gene of *S. coelicolor* or a homologue thereof, the method comprising functionally deleting in an antibiotic-producing strain of a *Streptomyces* species the *scbA* gene of *S. coelicolor* or a homologue thereof, culturing said strain under conditions suitable for the production of antibiotic, and determining whether antibiotic production in said strain is increased.

16. (original): A method for producing an antibiotic, the method comprising, following identification of a *Streptomyces* species according to claim 15, providing a strain of said species having a functional deletion of said *scbA* gene of *S. coelicolor* or homologue thereof, and culturing said strain under conditions suitable for antibiotic production.

17. (previously presented): The method of claim 16, further comprising the step of purifying the antibiotic from the culture medium.

18. (original): The method of claim 17, further comprising the step of formulating the antibiotic as a pharmaceutical.

19. (currently amended):The method of claim 15, wherein the *scbA* gene or homologue thereof has a nucleotide sequence which:

(a) is the complement of nucleotides 2914 to 1970 of EMBL AJ007731;

(b) is the complement of nucleotides 2142-1199 of ~~Fig. 14~~ SEQ ID NO: 19;

(c) encodes a polypeptide having at least about 35% sequence identity with ~~the amino acid sequence of Fig. 10~~ SEQ ID NO: 17; and/or

(d) is capable of specific hybridisation with the amplification product obtained using the primers:

oligo1 (5'-GACCACGT(CG)CC(CG)GGCATG; SEQ ID NO: 1) and

oligo2 (5'-GTCCTG(CG)TGGCC(CG)GT(CG)AC(CG)CG(CG)AC; SEQ ID NO: 2)

to amplify total DNA of said species or strain.

~~21~~20. (currently amended): The method of claim ~~20~~19, wherein the level of sequence identity is at least about 50%.

~~22~~21. (currently amended): The method of claim ~~21~~20, wherein the level of sequence identity is at least about 65%.

~~23~~22. (currently amended): The method of claim ~~22~~21, wherein the level of sequence identity is at least about 80%.

~~24~~23. (currently amended): The method of claim ~~23~~22, wherein the level of sequence identity is at least about 95%.

~~25~~24. (currently amended): A method for identifying *Streptomyces* species in which the timing of antibiotic production is altered by functionally deleting the *scbR* gene of *S. coelicolor* or a homologue thereof, the method comprising functionally deleting in an antibiotic-producing strain of a *Streptomyces* species the *scbR* gene of *S. coelicolor* or a homologue thereof, culturing said strain under conditions suitable for the production of antibiotic, and determining whether the timing of antibiotic production in said strain is altered.

~~26~~25. (currently amended): A method for producing an antibiotic, the method comprising, following identification of a *Streptomyces* species according to claim ~~25~~24, providing a strain of said species having a functional deletion of said *scbR* gene of *S. coelicolor* or homologue thereof, and culturing said strain under conditions suitable for antibiotic production.

26. (currently amended): The method of claim ~~22~~25, further comprising the step of purifying the antibiotic from the culture medium.

27. (currently amended): The method of claim ~~23~~26, further comprising the step of formulating the antibiotic as a pharmaceutical.

28. (currently amended): The method of claim ~~25~~24, wherein the *scbR* gene or homologue thereof:

(a) has a nucleotide sequence which is nucleotides 3032 to 3679 of EMBL AJ007731;

(b) has a nucleotide sequence which is nucleotides 2261-2908 of ~~Fig. 14~~ SEQ ID NO: 19;

(c) has a nucleotide sequence which encodes a polypeptide having at least about 35% sequence identity with ~~the amino acid sequence of Fig. 9~~ SEQ ID NO: 16; and/or

(d) is adjacent to and divergent from a gene which is capable of specific hybridisation with the amplification product obtained using the primers:

oligo1 (5'-GACCACGT(CG)CC(CG)GGCATG; SEQ ID NO: 1) and

oligo2 (5'-GTCCTG(CG)TGGCC(CG)GT(CG)AC(CG)CG(CG)AC; SEQ ID NO: 2) to amplify total DNA of said species or strain.

29. (original): The method of claim 28, wherein the level of sequence identity is at least about 50%.

30. (original): The method of claim 29, wherein the level of sequence identity is at least about 65%.

31. (original): The method of claim 30, wherein the level of sequence identity is at least about 80%.

32. (original): The method of claim 31, wherein the level of sequence identity is at least about 95%.